

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2002, 16:48:39 ; Search time 4873.04 Seconds
(without alignments)
1604.679 Million cell updates/sec

Title: US-09-236-995D-3
Perfect score: 474
Sequence: 1 acaagatgctattatggca.....gtttccatcacaaagaggtag 474

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.om.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.sy.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htgo_hum.*
- 31: em.htgo_inv.*
- 32: em.htgo_rod.*
- 33: em.htg_hum.*
- 34: em.htg_inv.*
- 35: em.htg_rod.*
- 36: em.htg_other.*

Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	474	100.0	3211	8	ZMPARP2	AJ222589 Zea mays
2	474	100.0	3285	8	AF093627	AF093627 Zea mays
3	280	59.1	3187	8	ATH131705	ATH131705 Arabidops
4	158.6	33.5	1939	10	RNPARP2	X65457 R.norvegicu
5	157.6	33.2	3718	5	XELPADPRP	D14667 Frog mrna f
6	157	33.1	3128	10	RNU94340	U94340 Rattus norv
7	155	32.7	3617	5	XLPARP	Z12139 X.laavis PA
8	154.4	32.6	2147	8	ATPARP	Z48243 A.thaliana
9	153.8	32.4	3036	5	GGPADPRP	X52690 Chicken mRN
10	152.2	32.1	3845	10	BC012041	BC012041 Mus muscu
11	151.4	31.9	2295	8	ZMPARP1	AJ222588 Zea mays
12	150.6	31.8	3172	10	NMADPRP	X14206 Mouse mrna
13	150.6	31.8	3589	4	BOVPAS	D90073 Bovine poly
14	149	31.4	1732	10	AF126717	AF126717 Mus muscu
15	147.4	31.1	3047	10	AF168781	AF168781 Crictetulu
16	142.6	30.1	1771	9	HUMADPPO	M17081 Human place
17	142.6	30.1	3640	9	HUMPOLP	M18112 Human poly(
18	142.6	30.1	3792	6	A52134	A52134 Sequence 1
19	142.6	30.1	3795	9	HUMRISDAD	J03473 Human poly(
20	142.6	30.1	5787	9	GORADPRB	L24094 Gorilla gor
21	139.4	29.4	3045	6	AX058340	AX058340 Sequence
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24	139.4	29.4	1822	3	DMPARP5	I14359 Sequence 5
25	137.8	29.1	2682	9	S54638	AF051548 drosophil
26	137.8	29.1	3080	3	DROADPRPA	S54638 pseudogene
27	137.8	29.1	5345	6	I14360	D13806 Fruit fly m
28	137.8	29.1	9254	9	HUMPADPRP2	I14360 Sequence 7
29	137.8	29.1	10988	2	AC014613	L14752 Homo sapien
30	137.8	29.1	16864	3	AE002892	AC014613 Drosophil
31	137.8	29.1	155026	9	AL442128	AE002892 Drosophil
32	137.8	29.0	3463	3	SPRADPRP	AL442128 Human DNA
33	137.4	28.7	2682	6	I14357	D16482 Sarcophaga
34	136.2	28.7	687	6	AX058382	I14357 Sequence 3
35	122.6	25.9	738	6	AX058380	AX058382 Sequence
36	122.6	25.9	864	6	AX058336	AX058380 Sequence
37	122.6	25.9	1754	9	HS236912	AX058336 Sequence
38	122.6	25.9	1797	9	HS236876	AJ236912 Homo sapi
39	122.6	25.9	1814	6	AX058317	AJ236876 Homo sapi
40	122.6	25.9	1843	6	AX008892	AX058317 Sequence
41	122.6	25.9	1874	6	AX058374	AX008892 Sequence
42	122.6	25.9	3200	6	AX058362	AX058374 Sequence
43	122.6	25.9	1910	9	AF085734	AX058362 Sequence
44	121	25.5	1707	6	AX058338	AF085734 Homo sapi
45	120.2	25.4	1707	6	AX058338	AX058338 Sequence

ALIGNMENTS

RESULT	1	ZMPARP2	ZMPARP2	3211 bp	mrna	PLN	19-NOV-1997
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
REFERENCE							
AUTHORS							
TITLE							

JOURNAL Submitted (14-NOV-1997) Kushnir S., VIB, Dep. Genetics,
Ledegeanckstraat 35, Gent, B9000, Belgium

FEATURES
source Location/Qualifiers
1. 3211
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113. 3022
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/codon_start=1
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/db_xref="GI:2632129"
/db_xref="SPREMBL:O24570"
/translation="MAAPPRKAWAEYAKSGRACKSCRSPIAKDQLRLGKMWQASQFD
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BASE COUNT 968 a 604 c 813 g 826 t

ORIGIN

Query Match 100.0%; Score 474; DB 8; Length 3211;
Best Local Similarity 100.0%; Pred. No. 9.2e-139;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2549 AACAAAGATGCTATTATGGCACGGTTCAAGGTGACGAATTTTGTGGGAATCTTAGTCAA 2608
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QY 61 gggctaaagattgacacctctgagcagcctgttactggtctatatgttcggcaaggcctc 120
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Db 2609 GGGCTAAGAAATGCACTCCTGAGGCACCTGTTACTGGCTATATGTTGGCAAAAGGCCTC 2668
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QY 121 tactttgcagatctagtaagcaagagcgcaacaatacttattgtggataggaataatctc 180
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Db 2669 TACTTTGCAGATCTAGTAGCAAGAGCGCACAACTACTGTTATGTGGATAGGAATAATCCT 2728
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QY 181 gtagggttgatgctctcttctgaggttcttaggagacatgtatgaactaaagaaagcc 240
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QY 241 acgtccatgacaaacctccaaagagggaagcattcagcgaaggattaggcaaacccgtg 300
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Db 2789 ACSTCCATGACAAACCTCCAAAGAGGGAAGCATTCGACCAAGGGATTAGGCAAAACCCGTG 2848
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QY 301 ccactgagtcagagtttgaagtggaggataatgctagttccctgcggcaagccg 360
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Db 2849 CCACGTGAGTCAGAGTTTGTGAAGTGGAGGATGATGTCGTAGTTCCTCGGCAAGCCG 2908
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QY 361 gtgccatcaatcattaggagctctgaactcatgatacagatgatacgtctcaaacaca 420
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Db 2909 GTGCCATCAATATTAGGAGCTCTGAACATCATGTACATGATGATGATGATGATGATGATGAT 4268
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QY 421 tcccagggtgaagatgaagttcttctgtaagggtgcgtttccatcacaagaggtag 474
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Db 2969 TCCCAGGTGAAGATGAGTCTTCTGCTGAAGGTGCGCTTTCCATCATCAAGAGGTAG 3022
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RESULT 2
AF093627 3285 bp mRNA PLN 29-NOV-1998
LOCUS Zea mays poly(ADP-ribose) polymerase (PARP1) mRNA, complete cds.
DEFINITION AF093627
ACCESSION AF093627
KEYWORDS Zea mays.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1. (bases 1 to 3285)
Mahajan, P.B. and Zuo, Z.
Purification and cDNA cloning of maize Poly(ADP-ribose) polymerase
Plant Physiol. 118 (3), 893-905 (1999)
99026291
2. (bases 1 to 3285)
Mahajan, P.B. and Zuo, Z.
Direct Submission
Submitted (22-SEP-1998) Crop Protection, Pioneer HiBred
International, Inc., 7300 NW 62nd Avenue, Johnston, IA 50131-1004,
USA
Location/Qualifiers
1. 3285
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/db_xref="taxon:4577"
1. 3285
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Query Match 100.0%; Score 474; DB 8; Length 3285;
Best Local Similarity 100.0%; Pred. No. 9.3e-139;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2569 AACAAAGATGCTATTATGGCACGGTTCAAGGTGACGAATTTTGTGGGAATCTTAGTCAA 2628
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 QY 2758 ggaattaggcaaacaccctgccactggagtgcagagtttgaaagtggaggatgatgtccta 2817
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 Db 2911 GTTCCCTCGCGGAAGCCGCTGCCATCATCAATTAGGAGCTCTGAACATCATGTACAATGAG 2970
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 Db 2971 TACATCGTCTACAAACACATCCCCAGGTGAAGATGCAGTCTTGTGCTGAAGGTCGCTTCCAT 3030
 QY 2938 cacaagaggtag 2949
 Db 3031 CACAAGAGGTAG 3042

RESULT 2
ZMPARP2
LOCUS ZMPARP2 3211 bp mRNA PLN 19-NOV-1997
DEFINITION Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).
ACCESSION AJ222589
VERSION AJ222589.1 GI:2632128
KEYWORDS PARP gene; poly(ADP-ribose) polymerase.
SOURCE Zea mays.
ORGANISM Zea mays;
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACU
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS 1 (bases 1 to 3211)
 Babyichuk E., Cottrill P., Storozhenko S., Fuangthong M.,
 O'Farrell M., Van Montagu M., Inze D. and Kushnir S.
 Higher plants possess two poly(ADP-ribose) polymerases
 Unpublished
 2 (bases 1 to 3211)
 Kushnir S.
 Direct Submission
 Submitted (14-NOV-1997) Kushnir S., VIB, Dep.Genetics,
 Ledeganckstraat 35, Gent, B9000, Belgium

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
FEATURES
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BASE COUNT 968 a 604 c 813 g 826 t
ORIGIN

Query Match 92.2%; Score 2720; DB 8; Length 3211;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2869; Conservative 22; Mismatches 16; Indels 45; Gaps 11;

Qy 1 atggcgccgcgcgaagcggtggaagcgagtgatcccaagtcgtggcgccgtcgatgc 60
Db 113 ATGGCGCGCGCCGAAAGCGGTGAAGCGGAGTATGCCAAGTCGGCGCGCGCTCGTGC 172
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Qy 121 tcacagttcgacggttcctccatgccgatgtggaaccatgccaggtgcattcttcagcaagaag 180
Db 233 TCACAGTTCGAGCGCTTCATGCCGATGTGGAACCATGCCAG----- 273
Qy 181 aaccagataaaatccgttgacatgttggaagggatagatgcacttagatgggatgacaa 240
Db 274 -----CGTTGACGATTTGAAGGGATAGATGCACCTAGATGGGATGATCAA 319
Qy 241 gagaagatacgaactacgttggagtgccctcagctggtacaaagtcttcacagctgctcc 300
Db 320 GAGAAGATACGAACACTAGCTTGGGNGTCCCTCAGCTGGTACAAAGTCTACAGCTGCTCT 379
Qy 301 cctgagaatgtacaaatgagatgtccatctgcccgtaccttcatttagacgagtcaggt 360
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Db 1460 GAATGTGTTAAAAGAACAAATGCTGCCATTTGATTTGATATAACTAGAGAAATGCCCTTA 1519
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Qy 1498 agtcctcyggtttgcaagaataactcactcattcctttagratggaaaagatacaaa 1557
Db 1578 AGTCTCTGTTGTGAAGA-TACTGCTCACAAT-CTTGAAGATGGGAAAGCATATACAA 1635
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RESULT 3
ATH131705
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DEFINITION Arabidopsis thaliana mRNA for poly(ADP-ribose) polymerase.
ACCESSION AJ131705
18-DEC-1998
PLN

VERSION AJ131705.1 GI:4038490
KEYWORDS NAD(+) ADP-ribosyltransferase; parp-1 gene; poly(ADP-ribose) polymerase.
SOURCE Arabidopsis thaliana
ORGANISM thale cress.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 3187)
AUTHORS Kazmaier, M.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie Vegetale Et De Microbiologie, Commissariat A L'Energie Atomique, CEA Cadarache, Lab. De Radiobiol. Vegetale, Bat. 185, 13108 St. Paul-les-Durance, FRANCE
AUTHORS Doucet-chabeaud, G. and Kazmaier, M.
JOURNAL Unpublished
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